

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Lee, Se-Jin
Huynh, Thanh
- (ii) TITLE OF THE INVENTION: GROWTH DIFFERENTIATION FACTOR-5
- (iii) NUMBER OF SEQUENCES: 27
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: Fish & Richardson, P.C.
 - (B) STREET: 4225 Executive Square, Suite 1400
 - (C) CITY: La Jolla
 - (D) STATE: CA
 - (E) COUNTRY: USA
 - (F) ZIP: 92037
-
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: Windows95
 - (D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER: 08/455,559
 - (B) FILING DATE: 31-MAY-1995
- (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER: 08/003,144
 - (B) FILING DATE: 12-JAN-1993
- (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: Lisa A. Haile, Ph.D.
 - (B) REGISTRATION NUMBER: 38,347
 - (C) REFERENCE/DOCKET NUMBER: 07265/057001
- (ix) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: 619/678-5070
 - (B) TELEFAX: 619/678-5099

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(vii) IMMEDIATE SOURCE:

(B) CLONE: 136

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CCGGAATTCG GNTGGGARMG NTGGRTNR

28

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 42 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(vii) IMMEDIATE SOURCE:

(B) CLONE: 121

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1..42

(C) OTHER INFORMATION: / N at residue 13, 25 and 28 = Inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CCGGAATTCT CANCCRCAYT CRTCNACNAC CATRTCYTCT TA

42

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:

(B) CLONE: 136

(ix) FEATURE:

(B) LOCATION: 1..7

(C) OTHER INFORMATION: Xaa at residue 4 = Arg or Ser; Xaa at residue 6 and 7 = Val, Ile or Met

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Gly Trp Glu Xaa Trp Xaa Xaa

1

5

1. The first of these is the fact that the
 2. second of these is the fact that the
 3. third of these is the fact that the
 4. fourth of these is the fact that the
 5. fifth of these is the fact that the
 6. sixth of these is the fact that the
 7. seventh of these is the fact that the
 8. eighth of these is the fact that the
 9. ninth of these is the fact that the
 10. tenth of these is the fact that the

- (ii) MOLECULE TYPE: peptide
- (vii) IMMEDIATE SOURCE:
- (B) CLONE: 121

Tyr Glu Asp Met Val Val Asp Glu Cys Gly Cys
1 5 10

CCGGAATTCG GNTGGVANRA YTGGRNRTN KCNCC

35

- ```
(ii) MOLECULE TYPE: Genomic DNA

(vii) IMMEDIATE SOURCE:
 (B) CLONE: 141

(ix) FEATURE:
 (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 1..35
 (C) OTHER INFORMATION: N at residue 12, 27, 30 and 33 = Inosine
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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CCGGAATTCG GNTGGVANRA YTGGRTNRTN KCNCC

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:  
(B) CLONE: 145

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence  
(B) LOCATION: 1..33  
(C) OTHER INFORMATION: N at residue 13, 19, 25 and 28 = Inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CCGGAATTCT CANSRCANG MNTCNACNRY CAT

33

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:

- (B) CLONE: 141

(ix) FEATURE:

- (B) LOCATION: 1..9  
(C) OTHER INFORMATION: Xaa at residue 3 = His, Gln, Asn, Lys, Glu or Asp; Xaa at residue 4 = Asp or Asn; Xaa at residues 6 and 7 = Val, Ile or Met; Xaa at residue 8 = Glu or Ser

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Gly Trp Xaa Xaa Trp Xaa Xaa Xaa Pro  
1 5

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:

- (B) CLONE: 145

(ix) FEATURE:

- (B) LOCATION: 1..8
- (C) OTHER INFORMATION: Xaa at residues 2 and 3 = Val, Ile, Met, Thr or Ala; Xaa at residue 4 = Asp or Glu; Xaa at residue 5 = Ala or Ser; Xaa at residue 7 = Gly, Ala, Arg, Asn, Asp, Cys, Glu, Gln, His, Ile, Leu, Lys, Met, Phe Pro, Ser, Thr, Trp, Tyr, and Val.

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Xaa Xaa Xaa Xaa Cys Xaa Cys  
1 5

## (2) INFORMATION FOR SEQ ID NO:9:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2329 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vii) IMMEDIATE SOURCE:

- (B) CLONE: GD-5

## (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence  
(B) LOCATION: 322...1806

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

|                                                                     |     |
|---------------------------------------------------------------------|-----|
| TTCAAGCCCT CAGTCAGTTG TGC GGGAGAA AGGGGGCGGT CGGCTTTCTC CTTTCAAGAA  | 60  |
| CGAGTTATTT TCAGCTGCTG ACTGGAGACG GTGCACGTCT GGACACGGGA GCACTTCCAC   | 120 |
| TATGGGACTG GATACAGACA CACGCCCGGC GGA CTTCAAG A CACTCAGAC TGAGGAGAAA | 180 |
| GCCCTGCCTG CTGCTGCTGC TGCTGCTGCT GCCACCGCTG CCTCTGAAGA CCCACTCCTT   | 240 |
| TCATGGTTTT TCCTGCCAAG CCAGAGGCAC CTTGCTGCT ACGGCCTTTC TCTGTGGTGT    | 300 |
| CATTCAGCGG CTGGCCAGAG G ATG AGA CTC CCC AAA CTC CTC ACT CTT TTG     | 351 |
| Met Arg Leu Pro Lys Leu Leu Thr Leu Leu                             |     |
| 1 5 10                                                              |     |
| CTG TGG CAC CTG GCT TGG CTG GAC CTG GAA CTC ATC TGC ACT GTG CTG     | 399 |
| Leu Trp His Leu Ala Trp Leu Asp Leu Glu Leu Ile Cys Thr Val Leu     |     |
| 15 20 25                                                            |     |
| GGT GCC CCT GAC TTA GGA CAG AGA ACC CCA GGG GCC AAG CCA GGG TTG     | 447 |
| Gly Ala Pro Asp Leu Gly Gln Arg Thr Pro Gly Ala Lys Pro Gly Leu     |     |
| 30 35 40                                                            |     |
| ACC AAA GCG GAG GCC AAG GAG AGG CCA CCC CTG GCC AGG AAT GTC TTT     | 495 |
| Thr Lys Ala Glu Ala Lys Glu Arg Pro Pro Leu Ala Arg Asn Val Phe     |     |
| 45 50 55                                                            |     |
| AGG CCA GGG GGT CAT ATC TAT GGT GTG GGG GCC ACC AAT GCC AGG GCC     | 543 |
| Arg Pro Gly Gly His Ile Tyr Gly Val Gly Ala Thr Asn Ala Arg Ala     |     |
| 60 65 70                                                            |     |
| AAG GGA AGC TCT GGG CAG ACA CAG GCC AAG AAG GAT GAA CCC AGA AAG     | 591 |
| Lys Gly Ser Ser Gly Gln Thr Gln Ala Lys Lys Asp Glu Pro Arg Lys     |     |
| 75 80 85 90                                                         |     |
| ATG CCC CCC AGA TCC GGT GGC TCT GAA ACC AAG CCA GGA CCC TCT TCC     | 639 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| Met | Pro | Pro | Arg | Ser | Gly | Gly | Ser | Glu | Thr | Lys | Pro | Gly | Pro | Ser | Ser |      |
|     |     |     |     | 95  |     |     |     |     | 100 |     |     |     |     | 105 |     |      |
| CAG | ACT | AGA | CAG | GCT | GCA | GCC | CGG | ACT | GTA | ACC | CCA | AAA | GGA | CAG | CTT | 687  |
| Gln | Thr | Arg | Gln | Ala | Ala | Ala | Arg | Thr | Val | Thr | Pro | Lys | Gly | Gln | Leu |      |
|     |     |     | 110 |     |     |     |     | 115 |     |     |     |     | 120 |     |     |      |
| CCT | GGG | GGC | AAA | GCA | TCT | TCA | AAA | GCA | GGA | TCT | GCC | CCC | AGC | TCC | TTC | 735  |
| Pro | Gly | Gly | Lys | Ala | Ser | Ser | Lys | Ala | Gly | Ser | Ala | Pro | Ser | Ser | Phe |      |
|     |     |     | 125 |     |     |     | 130 |     |     |     |     | 135 |     |     |     |      |
| CTG | CTG | AAG | AAG | ACC | AGG | GAG | CCT | GGG | ACC | CCT | CGA | GAG | CCC | AAG | GAG | 783  |
| Leu | Leu | Lys | Lys | Thr | Arg | Glu | Pro | Gly | Thr | Pro | Arg | Glu | Pro | Lys | Glu |      |
|     | 140 |     |     |     |     | 145 |     |     |     |     | 150 |     |     |     |     |      |
| CCG | TTC | CGC | CCG | CCC | CCC | ATC | ACA | CCC | CAC | GAA | TAC | ATG | CTC | TCC | CTG | 831  |
| Pro | Phe | Arg | Pro | Pro | Pro | Ile | Thr | Pro | His | Glu | Tyr | Met | Leu | Ser | Leu |      |
| 155 |     |     |     |     | 160 |     |     |     |     | 165 |     |     |     |     | 170 |      |
| TAC | AGG | ACG | CTG | TCC | GAT | GCT | GAC | AGA | AAG | GGA | GGT | AAC | AGC | AGC | GTG | 879  |
| Tyr | Arg | Thr | Leu | Ser | Asp | Ala | Asp | Arg | Lys | Gly | Gly | Asn | Ser | Ser | Val |      |
|     |     |     |     | 175 |     |     |     |     | 180 |     |     |     |     | 185 |     |      |
| AAG | TTG | GAG | GCT | GGC | CTG | GCC | AAC | ACC | ATC | ACC | AGC | TTT | ATT | GAC | AAA | 927  |
| Lys | Leu | Glu | Ala | Gly | Leu | Ala | Asn | Thr | Ile | Thr | Ser | Phe | Ile | Asp | Lys |      |
|     |     |     | 190 |     |     |     |     | 195 |     |     |     |     | 200 |     |     |      |
| GGG | CAA | GAT | GAC | CGA | GGC | CCT | GCG | GTC | AGG | AAG | CAG | AGG | TAC | GTG | TTT | 975  |
| Gly | Gln | Asp | Asp | Arg | Gly | Pro | Ala | Val | Arg | Lys | Gln | Arg | Tyr | Val | Phe |      |
|     |     | 205 |     |     |     |     | 210 |     |     |     |     | 215 |     |     |     |      |
| GAC | ATC | AGT | GCC | TTG | GAG | AAG | GAT | GGG | CTG | TTG | GGG | GCT | GAA | CTG | CGG | 1023 |
| Asp | Ile | Ser | Ala | Leu | Glu | Lys | Asp | Gly | Leu | Leu | Gly | Ala | Glu | Leu | Arg |      |
|     | 220 |     |     |     |     | 225 |     |     |     |     | 230 |     |     |     |     |      |
| ATC | TTA | CGG | AAG | AAG | CCC | TTG | GAC | GTG | GCC | AAG | CCA | GCG | GTC | CCC | AGT | 1071 |
| Ile | Leu | Arg | Lys | Lys | Pro | Leu | Asp | Val | Ala | Lys | Pro | Ala | Val | Pro | Ser |      |
| 235 |     |     |     |     | 240 |     |     |     |     | 245 |     |     |     |     | 250 |      |
| AGC | GGG | CGG | GTT | GCC | CAA | CTG | AAG | CTG | TCC | AGC | TGC | CCC | AGC | GGC | CGG | 1119 |
| Ser | Gly | Arg | Val | Ala | Gln | Leu | Lys | Leu | Ser | Ser | Cys | Pro | Ser | Gly | Arg |      |
|     |     |     |     | 255 |     |     |     |     | 260 |     |     |     |     | 265 |     |      |
| CAG | CCG | GCA | GCC | TTG | CTG | GAT | GTG | CGC | TCC | GTG | CCA | GGC | CTG | GAT | GGA | 1167 |
| Gln | Pro | Ala | Ala | Leu | Leu | Asp | Val | Arg | Ser | Val | Pro | Gly | Leu | Asp | Gly |      |
|     |     |     | 270 |     |     |     |     | 275 |     |     |     |     | 280 |     |     |      |
| TCT | GGC | TGG | GAG | GTG | TTC | GAC | ATC | TGG | AAG | CTC | TTC | CGA | AAT | TTT | AAG | 1215 |
| Ser | Gly | Trp | Glu | Val | Phe | Asp | Ile | Trp | Lys | Leu | Phe | Arg | Asn | Phe | Lys |      |
|     |     | 285 |     |     |     |     | 290 |     |     |     |     | 295 |     |     |     |      |
| AAC | TCA | GCG | CAG | CTG | TGC | CTG | GAG | CTG | GAG | GCC | TGG | GAA | CGG | GGC | CGG | 1263 |
| Asn | Ser | Ala | Gln | Leu | Cys | Leu | Glu | Leu | Glu | Ala | Trp | Glu | Arg | Gly | Arg |      |
|     | 300 |     |     |     |     | 305 |     |     |     |     | 310 |     |     |     |     |      |

|                                                                    |      |
|--------------------------------------------------------------------|------|
| GCC GTG GAC CTC CGT GGC CTG GGC TTT GAA CGC ACT GCC CGA CAG GTC    | 1311 |
| Ala Val Asp Leu Arg Gly Leu Gly Phe Glu Arg Thr Ala Arg Gln Val    |      |
| 315 320 325 330                                                    |      |
| CAC GAG AAA GCC TTG TTC CTA GTG TTT GGT CGT ACC AAG AAA CGG GAC    | 1359 |
| His Glu Lys Ala Leu Phe Leu Val Phe Gly Arg Thr Lys Lys Arg Asp    |      |
| 335 340 345                                                        |      |
| CTG TTC TTT AAT GAG ATT AAG GCC CGC TCT GGC CAG GAT GAC AAG ACT    | 1407 |
| Leu Phe Phe Asn Glu Ile Lys Ala Arg Ser Gly Gln Asp Asp Lys Thr    |      |
| 350 355 360                                                        |      |
| GTG TAT GAA TAT TTG TTC AGC CAG CGG CGG AAA CGC CGG GCC CCA TTG    | 1455 |
| Val Tyr Glu Tyr Leu Phe Ser Gln Arg Arg Lys Arg Arg Ala Pro Leu    |      |
| 365 370 375                                                        |      |
| GCC AAT CGC CAG GGC AAG CGA CCC AGC AAG AAC CTC AAG GCT CGC TGC    | 1503 |
| Ala Asn Arg Gln Gly Lys Arg Pro Ser Lys Asn Leu Lys Ala Arg Cys    |      |
| 380 385 390                                                        |      |
| AGT CGC AAG GCC TTG CAT GTC AAC TTC AAG GAC ATG GGC TGG GAC GAC    | 1551 |
| Ser Arg Lys Ala Leu His Val Asn Phe Lys Asp Met Gly Trp Asp Asp    |      |
| 395 400 405 410                                                    |      |
| TGG ATC ATC GCA CCT CTT GAG TAT GAG GCC TTC CAC TGC GAA GGA CTG    | 1599 |
| Trp Ile Ile Ala Pro Leu Glu Tyr Glu Ala Phe His Cys Glu Gly Leu    |      |
| 415 420 425                                                        |      |
| TGT GAG TTC CCC TTG CGC TCC CAC TTG GAG CCC ACA AAC CAC GCA GTC    | 1647 |
| Cys Glu Phe Pro Leu Arg Ser His Leu Glu Pro Thr Asn His Ala Val    |      |
| 430 435 440                                                        |      |
| ATT CAG ACC CTA ATG AAC TCT ATG GAC CCT GAA TCC ACA CCA CCC ACT    | 1695 |
| Ile Gln Thr Leu Met Asn Ser Met Asp Pro Glu Ser Thr Pro Pro Thr    |      |
| 445 450 455                                                        |      |
| TGT TGT GTG CCT ACA CGG CTG AGT CCT ATT AGC ATC CTC TTC ATC GAC    | 1743 |
| Cys Cys Val Pro Thr Arg Leu Ser Pro Ile Ser Ile Leu Phe Ile Asp    |      |
| 460 465 470                                                        |      |
| TCT GCC AAC AAC GTG GTG TAT AAA CAG TAC GAG GAC ATG GTC GTG GAA    | 1791 |
| Ser Ala Asn Asn Val Val Tyr Lys Gln Tyr Glu Asp Met Val Val Glu    |      |
| 475 480 485 490                                                    |      |
| TCT TGT GGC TGC AGG TAGCAGCACC GGCCACCTG TCTTCCAGGG TGGCACATCC A   | 1847 |
| Ser Cys Gly Cys Arg                                                |      |
| 495                                                                |      |
| GAGACTACCC CCTCTACAGG TTCCTGGAGT AACAGAGAGC CTGTGAAGCT GCTGCCCCGAA | 1907 |
| GTTTCCTGGC AGCCTGCAGG AAAGAGTTCT CAGCAGGCTT ACTCTCTGGA TGTGATCTGG  | 1967 |
| ACTAAAGAGA TCACCTTCTG AAGATTCTTG CCCAAGGAAC AGACTCTGAG TGGGCTGGG   | 2027 |
| GCTCAGGAAA GGTGTTCTTA ATGAGATTCA GTTCACCATC TCTCCTGCCG GGGCCGGAGA  | 2087 |
| CCTTCATTTT TCTCCAGACT CTCCAGAGAA GTTGTAGCTA TATCCTAAGC TCTTTAAGGG  | 2147 |
| AGAGCTGTCT CCTCCTTGAA TCACCTTTGT GCCTGGTGAC TTTCTGCCAC GAGATGTTCA  | 2207 |
| TTACAGGGGC TGGGCAAAGA AGGGGAAAGG GCTTGGGCAG GGGTGAAGAG AAGAGTATGA  | 2267 |

GCCTAATTAG ACTGTTAGAT TAAAATGTAC ATCGATGACA TAAAAGCTGA ATCTTCATGG 2327  
CT 2329

## (2) INFORMATION FOR SEQ ID NO:10:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 495 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (v) FRAGMENT TYPE: internal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Arg | Leu | Pro | Lys | Leu | Leu | Thr | Leu | Leu | Leu | Trp | His | Leu | Ala | Trp |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Leu | Asp | Leu | Glu | Leu | Ile | Cys | Thr | Val | Leu | Gly | Ala | Pro | Asp | Leu | Gly |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gln | Arg | Thr | Pro | Gly | Ala | Lys | Pro | Gly | Leu | Thr | Lys | Ala | Glu | Ala | Lys |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Glu | Arg | Pro | Pro | Leu | Ala | Arg | Asn | Val | Phe | Arg | Pro | Gly | Gly | His | Ile |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Tyr | Gly | Val | Gly | Ala | Thr | Asn | Ala | Arg | Ala | Lys | Gly | Ser | Ser | Gly | Gln |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Thr | Gln | Ala | Lys | Lys | Asp | Glu | Pro | Arg | Lys | Met | Pro | Pro | Arg | Ser | Gly |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gly | Ser | Glu | Thr | Lys | Pro | Gly | Pro | Ser | Gln | Thr | Arg | Gln | Ala | Ala |     |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Ala | Arg | Thr | Val | Thr | Pro | Lys | Gly | Gln | Leu | Pro | Gly | Gly | Lys | Ala | Ser |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ser | Lys | Ala | Gly | Ser | Ala | Pro | Ser | Ser | Phe | Leu | Leu | Lys | Lys | Thr | Arg |
|     | 130 |     |     |     |     | 135 |     |     |     | 140 |     |     |     |     |     |
| Glu | Pro | Gly | Thr | Pro | Arg | Glu | Pro | Lys | Glu | Pro | Phe | Arg | Pro | Pro | Pro |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Ile | Thr | Pro | His | Glu | Tyr | Met | Leu | Ser | Leu | Tyr | Arg | Thr | Leu | Ser | Asp |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ala | Asp | Arg | Lys | Gly | Gly | Asn | Ser | Ser | Val | Lys | Leu | Glu | Ala | Gly | Leu |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ala | Asn | Thr | Ile | Thr | Ser | Phe | Ile | Asp | Lys | Gly | Gln | Asp | Asp | Arg | Gly |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Pro | Ala | Val | Arg | Lys | Gln | Arg | Tyr | Val | Phe | Asp | Ile | Ser | Ala | Leu | Glu |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Lys | Asp | Gly | Leu | Leu | Gly | Ala | Glu | Leu | Arg | Ile | Leu | Arg | Lys | Lys | Pro |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Leu | Asp | Val | Ala | Lys | Pro | Ala | Val | Pro | Ser | Gly | Arg | Val | Ala | Gln |     |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     | 255 |     |     |
| Leu | Lys | Leu | Ser | Cys | Pro | Ser | Gly | Arg | Gln | Pro | Ala | Ala | Leu | Leu |     |
|     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |     |
| Asp | Val | Arg | Ser | Val | Pro | Gly | Leu | Asp | Gly | Ser | Gly | Trp | Glu | Val | Phe |
|     | 275 |     |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Asp | Ile | Trp | Lys | Leu | Phe | Arg | Asn | Phe | Lys | Asn | Ser | Ala | Gln | Leu | Cys |



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 290 |     | 295 |     | 300 |     |     |     |     |     |     |     |     |     |     |     |
| Leu | Glu | Leu | Glu | Ala | Trp | Glu | Arg | Gly | Arg | Ala | Val | Asp | Leu | Arg | Gly |
| 305 |     |     |     | 310 |     |     |     |     |     | 315 |     |     |     |     | 320 |
| Leu | Gly | Phe | Glu | Arg | Thr | Ala | Arg | Gln | Val | His | Glu | Lys | Ala | Leu | Phe |
|     |     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |
| Leu | Val | Phe | Gly | Arg | Thr | Lys | Lys | Arg | Asp | Leu | Phe | Phe | Asn | Glu | Ile |
|     |     |     | 340 |     |     |     |     |     | 345 |     |     |     |     | 350 |     |
| Lys | Ala | Arg | Ser | Gly | Gln | Asp | Asp | Lys | Thr | Val | Tyr | Glu | Tyr | Leu | Phe |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Ser | Gln | Arg | Arg | Lys | Arg | Arg | Ala | Pro | Leu | Ala | Asn | Arg | Gln | Gly | Lys |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Arg | Pro | Ser | Lys | Asn | Leu | Lys | Ala | Arg | Cys | Ser | Arg | Lys | Ala | Leu | His |
| 385 |     |     |     | 390 |     |     |     |     |     | 395 |     |     |     |     | 400 |
| Val | Asn | Phe | Lys | Asp | Met | Gly | Trp | Asp | Asp | Trp | Ile | Ile | Ala | Pro | Leu |
|     |     |     | 405 |     |     |     |     |     | 410 |     |     |     |     |     | 415 |
| Glu | Tyr | Glu | Ala | Phe | His | Cys | Glu | Gly | Leu | Cys | Glu | Phe | Pro | Leu | Arg |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |
| Ser | His | Leu | Glu | Pro | Thr | Asn | His | Ala | Val | Ile | Gln | Thr | Leu | Met | Asn |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |
| Ser | Met | Asp | Pro | Glu | Ser | Thr | Pro | Pro | Thr | Cys | Cys | Val | Pro | Thr | Arg |
|     | 450 |     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |
| Leu | Ser | Pro | Ile | Ser | Ile | Leu | Phe | Ile | Asp | Ser | Ala | Asn | Asn | Val | Val |
| 465 |     |     |     | 470 |     |     |     |     | 475 |     |     |     |     |     | 480 |
| Tyr | Lys | Gln | Tyr | Glu | Asp | Met | Val | Val | Glu | Ser | Cys | Gly | Cys | Arg |     |
|     |     |     |     | 485 |     |     |     |     | 490 |     |     |     |     | 495 |     |

## (2) INFORMATION FOR SEQ ID NO:11:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (vii) IMMEDIATE SOURCE:

- (B) CLONE: GDF-1

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Leu | Arg | Arg | His | Thr | Glu | Pro | Arg | Val | Glu | Val | Gly | Pro | Val | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Cys | Arg | Thr | Arg | Arg | Leu | His | Val | Ser | Phe | Arg | Glu | Val | Gly | Trp |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| His | Arg | Trp | Val | Ile | Ala | Pro | Arg | Gly | Phe | Leu | Ala | Asn | Phe | Cys | Gln |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Gly | Thr | Cys | Ala | Leu | Pro | Glu | Thr | Leu | Arg | Gly | Pro | Gly | Gly | Pro | Pro |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Ala | Leu | Asn | His | Ala | Val | Leu | Arg | Ala | Leu | Met | His | Ala | Ala | Ala | Pro |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     | 80  |
| Thr | Pro | Gly | Ala | Gly | Ser | Pro | Cys | Cys | Val | Pro | Glu | Arg | Leu | Ser | Pro |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Ile | Ser | Val | Leu | Phe | Phe | Asp | Asn | Glu | Asp | Asn | Val | Val | Leu | Arg | His |

```

 100 105 110
Tyr Glu Asp Met Val Val Asp Glu Cys Gly Cys Arg
 115 120

```

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

- (B) CLONE: GDF-3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

[illegible]

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

- (B) CLONE: GDF-5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Leu | Ala | Asn | Arg | Gln | Gly | Lys | Arg | Pro | Ser | Lys | Asn | Leu | Lys | Ala |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Arg | Cys | Ser | Arg | Lys | Ala | Leu | His | Val | Asn | Phe | Lys | Asp | Met | Gly | Trp |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|     | 20  |     | 25  |     | 30  |     |     |     |     |     |     |     |     |     |     |
| Asp | Asp | Trp | Ile | Ile | Ala | Pro | Leu | Glu | Tyr | Glu | Ala | Phe | His | Cys | Glu |
|     | 35  |     |     |     |     |     | 40  |     |     |     |     |     | 45  |     |     |
| Gly | Leu | Cys | Glu | Phe | Pro | Leu | Arg | Ser | His | Leu | Glu | Pro | Thr | Asn | His |
|     | 50  |     |     |     |     |     | 55  |     |     |     |     |     | 60  |     |     |
| Ala | Val | Ile | Gln | Thr | Leu | Met | Asn | Ser | Met | Asp | Pro | Glu | Ser | Thr | Pro |
|     | 65  |     |     |     |     |     | 70  |     |     |     | 75  |     |     |     | 80  |
| Pro | Thr | Cys | Cys | Val | Pro | Thr | Arg | Leu | Ser | Pro | Ile | Ser | Ile | Leu | Phe |
|     |     |     |     |     |     |     | 85  |     |     |     | 90  |     |     |     | 95  |
| Ile | Asp | Ser | Ala | Asn | Asn | Val | Val | Tyr | Lys | Gln | Tyr | Glu | Asp | Met | Val |
|     |     |     |     |     |     |     |     |     | 100 |     | 105 |     |     |     | 110 |
| Val | Glu | Ser | Cys | Gly | Cys | Arg |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     | 115 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

## (2) INFORMATION FOR SEQ ID NO:14:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (vii) IMMEDIATE SOURCE:

- (B) CLONE: GDF-9

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Phe | Asn | Leu | Ser | Glu | Tyr | Phe | Lys | Gln | Phe | Leu | Phe | Pro | Gln | Asn |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Glu | Cys | Glu | Leu | His | Asp | Phe | Arg | Leu | Ser | Phe | Ser | Gln | Leu | Lys | Trp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asp | Asn | Trp | Ile | Val | Ala | Pro | His | Arg | Tyr | Asn | Pro | Arg | Tyr | Cys | Lys |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gly | Asp | Cys | Pro | Arg | Ala | Val | Arg | His | Arg | Tyr | Gly | Ser | Pro | Val | His |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Thr | Met | Val | Gln | Asn | Ile | Ile | Tyr | Glu | Lys | Leu | Asp | Pro | Ser | Val | Pro |
|     | 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Arg | Pro | Ser | Cys | Val | Pro | Gly | Lys | Tyr | Ser | Pro | Leu | Ser | Val | Leu | Thr |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ile | Glu | Pro | Asp | Gly | Ser | Ile | Ala | Tyr | Lys | Glu | Tyr | Glu | Asp | Met | Ile |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ala | Thr | Arg | Cys | Thr | Cys | Arg |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     | 115 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

## (2) INFORMATION FOR SEQ ID NO:15:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

(B) CLONE: BMP-2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

```

Arg Glu Lys Arg Gln Ala Lys His Lys Gln Arg Lys Arg Leu Lys Ser
 1 5 10 15
Ser Cys Lys Arg His Pro Leu Tyr Val Asp Phe Ser Asp Val Gly Trp
 20 25 30
Asn Asp Trp Ile Val Ala Pro Pro Gly Tyr His Ala Phe Tyr Cys His
 35 40 45
Gly Glu Cys Pro Phe Pro Leu Ala Asp His Leu Asn Ser Thr Asn His
 50 55 60
Ala Ile Val Gln Thr Leu Val Asn Ser Val Asn Ser Lys Ile Pro Lys
 65 70 75 80
Ala Cys Cys Val Pro Thr Glu Leu Ser Ala Ile Ser Met Leu Tyr Leu
 85 90 95
Asp Glu Asn Glu Lys Val Val Leu Lys Asn Tyr Gln Asp Met Val Val
 100 105 110
Glu Gly Cys Gly Cys Arg
 115

```

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 118 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

(B) CLONE: BMP-4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

```

Lys Arg Ser Pro Lys His His Ser Gln Arg Ala Arg Lys Lys Asn Lys
 1 5 10 15
Asn Cys Arg Arg His Ser Leu Tyr Val Asp Phe Ser Asp Val Gly Trp
 20 25 30
Asn Asp Trp Ile Val Ala Pro Pro Gly Tyr Gln Ala Phe Tyr Cys His
 35 40 45
Gly Asp Cys Pro Phe Pro Leu Ala Asp His Leu Asn Ser Thr Asn His
 50 55 60
Ala Ile Val Gln Thr Leu Val Asn Ser Val Asn Ser Ser Ile Pro Lys
 65 70 75 80
Ala Cys Cys Val Pro Thr Glu Leu Ser Ala Ile Ser Met Leu Tyr Leu
 85 90 95
Asp Glu Tyr Asp Lys Val Val Leu Lys Asn Tyr Gln Glu Met Val Val
 100 105 110
Glu Gly Cys Gly Cys Arg

```

115

## (2) INFORMATION FOR SEQ ID NO:17:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (vii) IMMEDIATE SOURCE:

- (B) CLONE: Vgr-1

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Arg | Gly | Ser | Gly | Ser | Ser | Asp | Tyr | Asn | Gly | Ser | Glu | Leu | Lys | Thr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Cys | Lys | Lys | His | Glu | Leu | Tyr | Val | Ser | Phe | Gln | Asp | Leu | Gly | Trp |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Gln | Asp | Trp | Ile | Ile | Ala | Pro | Lys | Gly | Tyr | Ala | Ala | Asn | Tyr | Cys | Asp |
|     | 35  |     |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gly | Glu | Cys | Ser | Phe | Pro | Leu | Asn | Ala | His | Met | Asn | Ala | Thr | Asn | His |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ala | Ile | Val | Gln | Thr | Leu | Val | His | Leu | Met | Asn | Pro | Glu | Tyr | Val | Pro |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Lys | Pro | Cys | Cys | Ala | Pro | Thr | Lys | Leu | Asn | Ala | Ile | Ser | Val | Leu | Tyr |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Phe | Asp | Asp | Asn | Ser | Asn | Val | Ile | Leu | Lys | Lys | Tyr | Arg | Asn | Met | Val |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Val | Arg | Ala | Cys | Gly | Cys | His |     |     |     |     |     |     |     |     |     |
|     |     |     | 115 |     |     |     |     |     |     |     |     |     |     |     |     |

## (2) INFORMATION FOR SEQ ID NO:18:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (vii) IMMEDIATE SOURCE:

- (B) CLONE: OP-1

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Arg | Met | Ala | Asn | Val | Ala | Glu | Asn | Ser | Ser | Ser | Asp | Gln | Arg | Gln |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Cys | Lys | Lys | His | Glu | Leu | Tyr | Val | Ser | Phe | Arg | Asp | Leu | Gly | Trp |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Gln | Asp | Trp | Ile | Ile | Ala | Pro | Glu | Gly | Tyr | Ala | Ala | Tyr | Tyr | Cys | Glu |

```

 35 40 45
Gly Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met Asn Ala Thr Asn His
 50 55 60
Ala Ile Val Gln Thr Leu Val His Phe Ile Asn Pro Glu Thr Val Pro
 65 70 75 80
Lys Pro Cys Cys Ala Pro Thr Gln Leu Asn Ala Ile Ser Val Leu Tyr
 85 90 95
Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys Tyr Arg Asn Met Val
 100 105 110
Val Arg Ala Cys Gly Cys His
 115

```

## (2) INFORMATION FOR SEQ ID NO:19:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (vii) IMMEDIATE SOURCE:

- (B) CLONE: BMP-5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

```

Ser Arg Met Ser Ser Val Gly Asp Tyr Asn Thr Ser Glu Gln Lys Gln
 1 5 10 15
Ala Cys Lys Lys His Glu Leu Tyr Val Ser Phe Arg Asp Leu Gly Trp
 20 25 30
Gln Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala Ala Phe Tyr Cys Asp
 35 40 45
Gly Glu Cys Ser Phe Pro Leu Asn Ala His Met Asn Ala Thr Asn His
 50 55 60
Ala Ile Val Gln Thr Leu Val His Leu Met Phe Pro Asp His Val Pro
 65 70 75 80
Lys Pro Cys Cys Ala Pro Thr Lys Leu Asn Ala Ile Ser Val Leu Tyr
 85 90 95
Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys Tyr Arg Asn Met Val
 100 105 110
Val Arg Ser Cys Gly Cys His
 115

```

## (2) INFORMATION FOR SEQ ID NO:20:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

(B) CLONE: BMP-3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

```

Glu Gln Thr Leu Lys Lys Ala Arg Arg Lys Gln Trp Ile Glu Pro Arg
 1 5 10 15
Asn Cys Ala Arg Arg Tyr Leu Lys Val Asp Phe Ala Asp Ile Gly Trp
 20 25 30
Ser Glu Trp Ile Ile Ser Pro Lys Ser Phe Asp Ala Tyr Tyr Cys Ser
 35 40 45
Gly Ala Cys Gln Phe Pro Met Pro Lys Ser Leu Lys Pro Ser Asn His
 50 55 60
Ala Thr Ile Gln Ser Ile Val Arg Ala Val Gly Val Val Pro Gly Ile
 65 70 75 80
Pro Glu Pro Cys Cys Val Pro Glu Lys Met Ser Ser Leu Ser Ile Leu
 85 90 95
Phe Phe Asp Glu Asn Lys Asn Val Val Leu Lys Val Tyr Pro Asn Met
 100 105 110
Thr Val Glu Ser Cys Ala Cys Arg
 115 120

```

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 116 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vii) IMMEDIATE SOURCE:

(B) CLONE: MIS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

```

Gly Pro Gly Arg Ala Gln Arg Ser Ala Gly Ala Thr Ala Ala Asp Gly
 1 5 10 15
Pro Cys Ala Leu Arg Glu Leu Ser Val Asp Leu Arg Ala Glu Arg Ser
 20 25 30
Val Leu Ile Pro Glu Thr Tyr Gln Ala Asn Asn Cys Gln Gly Val Cys
 35 40 45
Gly Trp Pro Gln Ser Asp Arg Asn Pro Arg Tyr Gly Asn His Val Val
 50 55 60
Leu Leu Leu Lys Met Gln Ala Arg Gly Ala Ala Leu Ala Arg Pro Pro
 65 70 75 80
Cys Cys Val Pro Thr Ala Tyr Ala Gly Lys Leu Leu Ile Ser Leu Ser
 85 90 95
Glu Glu Arg Ile Ser Ala His His Val Pro Asn Met Val Ala Thr Glu
 100 105 110
Cys Gly Cys Arg
 115

```

## (2) INFORMATION FOR SEQ ID NO:22:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (vii) IMMEDIATE SOURCE:

- (B) CLONE: Inhibit-alpha

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Ala Leu Arg Leu Leu Gln Arg Pro Pro Glu Glu Pro Ala Ala His Ala  
 1 5 10 15  
 Asn Cys His Arg Val Ala Leu Asn Ile Ser Phe Gln Glu Leu Gly Trp  
 20 25 30  
 Glu Arg Trp Ile Val Tyr Pro Pro Ser Phe Ile Phe His Tyr Cys His  
 35 40 45  
 Gly Gly Cys Gly Leu His Ile Pro Pro Asn Leu Ser Leu Pro Val Pro  
 50 55 60  
 Gly Ala Pro Pro Thr Pro Ala Gln Pro Tyr Ser Leu Leu Pro Gly Ala  
 65 70 75 80  
 Gln Pro Cys Cys Ala Ala Leu Pro Gly Thr Met Arg Pro Leu His Val  
 85 90 95  
 Arg Thr Thr Ser Asp Gly Gly Tyr Ser Phe Lys Tyr Glu Thr Val Pro  
 100 105 110  
 Asn Leu Leu Thr Gln His Cys Ala Cys Ile  
 115 120

## (2) INFORMATION FOR SEQ ID NO:23:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (vii) IMMEDIATE SOURCE:

- (B) CLONE: Inhibit-beta-alpha

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

His Arg Arg Arg Arg Arg Gly Leu Glu Cys Asp Gly Lys Val Asn Ile  
 1 5 10 15  
 Cys Cys Lys Lys Gln Phe Phe Val Ser Phe Lys Asp Ile Gly Trp Asn  
 20 25 30  
 Asp Trp Ile Ile Ala Pro Ser Gly Tyr His Ala Asn Tyr Cys Glu Gly  
 35 40 45  
 Glu Cys Pro Ser His Ile Ala Gly Thr Ser Gly Ser Ser Leu Ser Phe  
 50 55 60



```

His Ser Thr Val Ile Asn His Tyr Arg Met Arg Gly His Ser Pro Phe
 65 70 75 80
Ala Asn Leu Lys Ser Cys Cys Val Pro Thr Lys Leu Arg Pro Met Ser
 85 90 95
Met Leu Tyr Tyr Asp Asp Gly Gln Asn Ile Ile Lys Lys Asp Ile Gln
 100 105 110
Asn Met Ile Val Glu Glu Cys Gly Cys Ser
 115 120

```

## (2) INFORMATION FOR SEQ ID NO:24:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (vii) IMMEDIATE SOURCE:

- (B) CLONE: Inhibit-beta-beta

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

```

His Arg Ile Arg Lys Arg Gly Leu Glu Cys Asp Gly Arg Thr Asn Leu
 1 5 10 15
Cys Cys Arg Gln Gln Phe Phe Ile Asp Phe Arg Leu Ile Gly Trp Asn
 20 25 30
Asp Trp Ile Ile Ala Pro Thr Gly Tyr Tyr Gly Asn Tyr Cys Glu Gly
 35 40 45
Ser Cys Pro Ala Tyr Leu Ala Gly Val Pro Gly Ser Ala Ser Ser Phe
 50 55 60
His Thr Ala Val Val Asn Gln Tyr Arg Met Arg Gly Leu Asn Pro Gly
 65 70 75 80
Thr Val Asn Ser Cys Cys Ile Pro Thr Lys Leu Ser Thr Met Ser Met
 85 90 95
Leu Tyr Phe Asp Asp Glu Tyr Asn Ile Val Lys Arg Asp Val Pro Asn
 100 105 110
Met Ile Val Glu Glu Cys Gly Cys Ala
 115 120

```

## (2) INFORMATION FOR SEQ ID NO:25:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (vii) IMMEDIATE SOURCE:

- (B) CLONE: TGF-beta-1

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

```

His Arg Arg Ala Leu Asp Thr Asn Tyr Cys Phe Ser Ser Thr Glu Lys
 1 5 10 15
Asn Cys Cys Val Arg Gln Leu Tyr Ile Asp Phe Arg Lys Asp Leu Gly
 20 25 30
Trp Lys Trp Ile His Glu Pro Lys Gly Tyr His Ala Asn Phe Cys Leu
 35 40 45
Gly Pro Cys Pro Tyr Ile Trp Ser Leu Asp Thr Gln Tyr Ser Lys Val
 50 55 60
Leu Ala Leu Tyr Asn Gln His Asn Pro Gly Ala Ser Ala Ala Pro Cys
 65 70 75 80
Cys Val Pro Gln Ala Leu Glu Pro Leu Pro Ile Val Tyr Tyr Val Gly
 85 90 95
Arg Lys Pro Lys Val Glu Gln Leu Ser Asn Met Ile Val Arg Ser Cys
 100 105 110
Lys Cys Ser
 115

```

## (2) INFORMATION FOR SEQ ID NO:26:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (vii) IMMEDIATE SOURCE:

- (B) CLONE: TGF-beta-2

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

```

Lys Lys Arg Ala Leu Asp Ala Ala Tyr Cys Phe Arg Asn Val Gln Asp
 1 5 10 15
Asn Cys Cys Leu Arg Pro Leu Tyr Ile Asp Phe Lys Arg Asp Leu Gly
 20 25 30
Trp Lys Trp Ile His Glu Pro Lys Gly Tyr Asn Ala Asn Phe Cys Ala
 35 40 45
Gly Ala Cys Pro Tyr Leu Trp Ser Ser Asp Thr Gln His Ser Arg Val
 50 55 60
Leu Ser Leu Tyr Asn Thr Ile Asn Pro Glu Ala Ser Ala Ser Pro Cys
 65 70 75 80
Cys Val Ser Gln Asp Leu Glu Pro Leu Thr Ile Leu Tyr Tyr Ile Gly
 85 90 95
Lys Thr Pro Lys Ile Glu Gln Leu Ser Asn Met Ile Val Lys Ser Cys
 100 105 110
Lys Cys Ser
 115

```

## (2) INFORMATION FOR SEQ ID NO:27:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (vii) IMMEDIATE SOURCE:

- (B) CLONE: TGF-beta-3

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Lys Lys Arg Ala Leu Asp Thr Asn Tyr Cys Phe Arg Asn Leu Glu Glu  
 1 5 10 15  
 Asn Cys Cys Val Arg Pro Leu Tyr Ile Asp Phe Arg Gln Asp Leu Gly  
 20 25 30  
 Trp Lys Trp Val His Glu Pro Lys Gly Tyr Tyr Ala Asn Phe Cys Ser  
 35 40 45  
 Gly Pro Cys Pro Tyr Leu Arg Ser Ala Asp Thr Thr His Ser Thr Val  
 50 55 60  
 Leu Gly Leu Tyr Asn Thr Leu Asn Pro Glu Ala Ser Ala Ser Pro Cys  
 65 70 75 80  
~~Cys Val Pro Gln Asp Leu Glu Pro Leu Thr Ile Leu Tyr Tyr Val Gly~~  
~~85 90 95~~  
 Arg Thr Pro Lys Val Glu Gln Leu Ser Asn Met Val Val Lys Ser Cys  
 100 105 110  
 Lys Cys Ser  
 115